



AMENDED SEQUENCE LISTING

<110> Zoghbi, Huda
Bellen, Hugo
Birmingham, Nessim
Hassan, Bessam
Ben-Arie, Nissim

<120> Compositions and Methods for Therapeutic Use of Atonal-associated Sequence for Deafness, Osteoarthritis, and Abnormal Cell Proliferation

<130> P01899US3

<140> US 09/980,381

<141> 2000-06-01

<150> US 60/137,060

<151> 1999-06-01

<150> US 60/176,993

<151> 2000-01-19

<150> PCT/US 00/15410

<151> 2000-06-01

<160> 70

<170> PatentIn version 3.1

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Tyr Pro Pro Glu Leu Ser Leu Leu Asp Ser Thr Asp Pro Arg Ala Trp
50 55 60

Leu Ala Pro Thr Leu Gln Gly Ile Cys Thr Ala Arg Ala Ala Gln Tyr
65 70 75 80

Leu Leu His Ser Pro Glu Leu Gly Ala Ser Glu Ala Ala Ala Pro Arg
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Ala Ser Ser Ser Lys Ser Pro Gly Pro Val Lys Val Arg Glu Gln Leu
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Cys Lys Leu Lys Gly Gly Val Val Val Asp Glu Leu Gly Cys Ser Arg
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Gln Arg Ala Pro Ser Ser Lys Gln Val Asn Gly Val Gln Lys Gln Arg
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Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn
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His Ala Phe Asp Gln Leu Arg Asn Val Ile Pro Ser Phe Asn Asn Asp
 180 185 190

Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile
 195 200 205

Asn Ala Leu Ser Glu Leu Leu Gln Thr Pro Ser Gly Gly Glu Gln Pro
 210 215 220

Pro Pro Pro Pro Ala Ser Cys Lys Ser Asp His His His Leu Arg Thr
 225 230 235 240

Ala Ala Ser Tyr Glu Gly Gly Ala Gly Asn Ala Thr Ala Ala Gly Ala
 245 250 255

Gln Gln Ala Ser Gly Gly Ser Gln Arg Pro Thr Pro Pro Gly Ser Cys
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Arg Thr Arg Phe Ser Ala Pro Ala Ser Ala Gly Gly Tyr Ser Val Gln
 275 280 285

Leu Asp Ala Leu His Phe Ser Thr Phe Glu Asp Ser Ala Leu Thr Ala
 290 295 300

Met Met Ala Gln Lys Asn Leu Ser Pro Ser Leu Pro Gly Ser Ile Leu
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35 40 45

Ala Glu Val Gly Asp Cys Arg Gly Thr Ser Arg Lys Leu Arg Ala Arg
50 55 60

Arg Gly Gly Arg Asn Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln
65 70 75 80

Arg Arg Ser Arg Arg Lys Lys Ala Asn Asp Arg Glu Arg Asn Arg Met
85 90 95

His Asn Leu Asn Ser Ala Leu Asp Ala Leu Arg Gly Val Leu Pro Thr
100 105 110

Phe Pro Asp Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala
115 120 125

His Asn Tyr Ile Trp Ala Leu Thr Gln Thr Leu Arg Ile Ala Asp His
130 135 140

Ser Phe Tyr Gly Pro Glu Pro Pro Val Pro Cys Gly Glu Leu Gly Ser
145 150 155 160

Pro Gly Gly Gly Ser Asn Gly Asp Trp Gly Ser Ile Tyr Ser Pro Val
165 170 175

Ser Gln Ala Gly Asn Leu Ser Pro Thr Ala Ser Leu Glu Glu Phe Pro
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Gly Leu Gln Val Pro Ser Ser Pro Ser Tyr Leu Leu Pro Gly Ala Leu
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Val Phe Ser Asp Phe Leu
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Gly Ser Ala Arg Gly Gln Arg Gly Ala Glu Ala Gly Gln Gly Val Gln
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Gly Ser Pro Ala Ser Gly Ala Gly Gly Cys Arg Pro Gly Arg Leu Leu
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Arg Arg Leu Lys Ala Asn Asn Arg Glu Arg Asn Arg Met His Asn Leu
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Asn Ala Ala Leu Asp Ala Leu Arg Glu Val Leu Pro Thr Phe Pro Glu
 130 135 140

Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala His Asn Tyr
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Ile Trp Ala Leu Thr Glu Thr Leu Arg Leu Ala Asp His Cys Ala Gly
 165 170 175

Ala Gly Gly Leu Gln Gly Ala Leu Phe Thr Glu Ala Val Leu Leu Ser
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Pro Gly Ala Ala Leu Gly Ala Ser Gly Asp Ser Pro Ser Pro Pro Ser
 195 200 205

Ser Trp Ser Cys Thr Asn Ser Pro Ala Ser Ser Ser Asn Ser Thr Ser
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Pro Tyr Ser Cys Thr Leu Ser Pro Ala Ser Pro Gly Ser Asp Val Asp
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Lys Arg Ala Pro Gly Glu Glu Thr Glu Lys Glu Glu Glu Glu Glu Asp
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65 70 75 80

Lys Lys Lys Thr Thr Lys Leu Arg Leu Glu Arg Val Lys Phe Arg Arg
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Gln Glu Ala Asn Ala Arg Glu Arg Asn Arg Met His Gly Leu Asn Asp
100 105 110

Ala Leu Asp Asn Leu Arg Lys Val Val Pro Cys Tyr Ser Lys Thr Gln
115 120 125

Lys Leu Ser Lys Ile Glu Thr Leu Arg Leu Ala Lys Asn Tyr Ile Trp
130 135 140

Ala Leu Ser Glu Ile Leu Arg Ile Gly Lys Arg Pro Asp Leu Leu Thr
145 150 155 160

Phe Val Gln Asn Leu Cys Lys Gly Leu Ser Gln Pro Thr Thr Asn Leu
165 170 175

Val Ala Gly Cys Leu Gln Leu Asn Ala Arg Ser Phe Leu Met Gly Gln
180 185 190

Gly Gly Glu Ala Ala His His Thr Arg Ser Pro Tyr Ser Thr Phe Tyr
195 200 205

Pro Pro Tyr His Ser Pro Glu Leu Ala Thr Pro Pro Gly His Gly Thr
210 215 220

Leu Asp Asn Ser Lys Ser Met Lys Pro Tyr Asn Tyr Cys Ser Ala Tyr
225 230 235 240

Glu Ser Phe Tyr Glu Ser Thr Ser Pro Glu Cys Ala Ser Pro Gln Phe
245 250 255

Glu Gly Pro Leu Ser Pro Pro Pro Ile Asn Tyr Asn Gly Ile Phe Ser
260 265 270

Leu Lys Gln Glu Glu Thr Leu Asp Tyr Gly Lys Asn Tyr Asn Tyr Gly
275 280 285

Met His Tyr Cys Ala Val Pro Pro Arg Gly Pro Leu Gly Gln Gly Ala
290 295 300

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 35 40 45

Ala Glu Leu Ser Leu Leu Asp Ser Thr Asp Pro Arg Ala Trp Leu Thr
 50 55 60

Pro Thr Leu Gln Gly Leu Cys Thr Ala Arg Ala Ala Gln Tyr Leu Leu
 65 70 75 80

His Ser Pro Glu Leu Gly Ala Ser Glu Ala Ala Ala Pro Arg Asp Glu
 85 90 95

Ala Asp Ser Gln Gly Glu Leu Val Arg Arg Ser Gly Cys Gly Gly Leu
 100 105 110

Ser Lys Ser Pro Gly Pro Val Lys Val Arg Glu Gln Leu Cys Lys Leu
 115 120 125

Lys Gly Gly Val Val Val Asp Glu Leu Gly Cys Ser Arg Gln Arg Ala
 130 135 140

Pro Ser Ser Lys Gln Val Asn Gly Val Gln Lys Gln Arg Arg Leu Ala
 145 150 155 160

Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn His Ala Phe
 165 170 175

Asp Gln Leu Arg Asn Val Ile Pro Ser Phe Asn Asn Asp Lys Lys Leu
 180 185 190

Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile Asn Ala Leu
 195 200 205

Ser Glu Leu Leu Gln Thr Pro Asn Val Gly Glu Gln Pro Pro Pro Pro
 210 215 220

Thr Ala Ser Cys Lys Asn Asp His His His Leu Arg Thr Ala Ser Ser
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Tyr Glu Gly Gly Ala Gly Ala Ser Ala Val Ala Gly Ala Gln Pro Ala
 245 250 255

Pro Gly Gly Gly Pro Arg Pro Thr Pro Pro Gly Pro Cys Arg Thr Arg
 260 265 270

Phe Ser Gly Pro Ala Ser Ser Gly Gly Tyr Ser Val Gln Leu Asp Ala
 275 280 285

Leu His Phe Pro Ala Phe Glu Asp Arg Ala Leu Thr Ala Met Met Ala
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Gln Lys Asp Leu Ser Pro Ser Leu Pro Gly Gly Ile Leu Gln Pro Val
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<220>
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 <223> n can be any nucleotide

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 <212> DNA
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<400> 14						
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 <211> 675
 <212> DNA
 <213> HUMAN

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<210> 16
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 <212> DNA
 <213> DROSPHILA

<220>
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 <223> n can be any nucleotide

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<210> 17
 <211> 189
 <212> PRT
 <213> DROSOPHILA

<400> 17

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Gly Gln Asp Tyr Gly Gln Gly Ala Phe Leu Ser Pro Glu Trp Gln Phe
 35 40 45

Leu Asp Ala Ala Gly Gly Thr Gln Thr Glu Leu Gly Pro Ile Met Glu
 50 55 60

Val Gln Gly Gln His Thr Gln Pro Gln Thr Lys Arg Arg Ser Asn Ser
 65 70 75 80

Ser Thr Gly Ser Asp Gly Arg Lys Ser Ser Pro Glu Gln Thr Asn Leu
 85 90 95

Ser Pro Thr Val Gln Lys Arg Arg Arg Gln Ala Ala Asn Ala Arg Glu
 100 105 110

Arg Lys Arg Met Asn Gly Leu Asn Ala Ala Phe Glu Arg Leu Arg Glu
 115 120 125

Val Val Pro Ala Pro Ser Ile Asp Gln Lys Leu Ser Lys Phe Glu Thr
 130 135 140

Leu Gln Met Ala Gln Ser Tyr Ile Leu Ala Leu Cys Asp Leu Leu Asn
 145 150 155 160

Asn Gly Asp Val Glu Val Asp Ala Ala Ala Tyr Thr Ile Phe Gly Asp
 165 170 175

Ser Asp Ser Gly Phe Gly Leu Ser Gly Gly Ser Leu Ser

180

185

<210> 18
 <211> 1074
 <212> DNA
 <213> CHICKEN

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<210> 19
 <211> 178
 <212> PRT
 <213> CHICKEN

<400> 19

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Ala Pro Arg Glu Arg Arg Arg Arg Arg Gly Arg Ala Arg Ala Arg Thr
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Glu Ala Leu Leu His Thr Leu Lys Arg Ser Arg Arg Val Lys Ala Asn
 35 40 45

Asp Arg Glu Arg Asn Arg Met His His Leu Asn Ala Ala Leu Asp Glu
 50 55 60

Leu Arg Ser Val Leu Pro Thr Phe Pro Asp Asp Thr Lys Leu Thr Lys
 65 70 75 80

Ile Glu Thr Leu Arg Phe Ala Tyr Asn Tyr Ile Trp Ala Leu Ser Glu
 85 90 95

Thr Leu Arg Leu Ala Glu Gln Cys Leu Pro Pro Pro Pro Ala Phe Arg
 100 105 110

Gly Pro Pro Ala Pro Pro Ser Pro Gly Ser Asp Ala Gly Ser Trp Leu
 115 120 125

Ser Ser Gly Ser Pro Ala Ala Pro Ser Leu Cys Ala Ser Ala Ser Gly
 130 135 140

145 150 155 160

Ala Leu Arg Ala Phe Arg Gly Leu Pro Pro Ala Ala Pro Gly Ala Pro
 165 170 175

Cys Arg

<210> 20
 <211> 790
 <212> DNA
 <213> CHICKEN

<400> 20
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<210> 21
 <211> 213
 <212> PRT
 <213> CHICKEN

<400> 21

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 20 25 30

Ser Ala Gly Glu Glu Asp Glu Asp Glu Glu Asp Gly Arg Pro Arg Arg
 35 40 45

Leu Gln Glu Gly Ala Arg Arg Ala Gly Arg Gln Arg Gly Pro Pro Arg
 50 55 60

Ala Ala Arg Thr Ala Glu Thr Ala Gln Arg Ile Lys Arg Ser Arg Arg
 65 70 75 80

Leu Lys Ala Asn Asn Arg Glu Arg Asn Arg Met His Asn Leu Asn Ala
 85 90 95

Ala Leu Asp Ala Leu Arg Asp Val Leu Pro Thr Phe Pro Glu Asp Ala
 100 105 110

Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala His Asn Tyr Ile Trp
 115 120 125

Ala Leu Thr Glu Thr Leu Arg Leu Ala Gly Ala Ala Arg Leu Gly Gly
 130 135 140

Ala Ala Asp Ala Ala Pro Gly Ala Ala Ala Glu Gly Ser Pro Ser Pro
 145 150 155 160

Ala Ser Ser Trp Ser Gly Gly Ala Ser Pro Ala Pro Ser Ala Ser Pro
 165 170 175

Tyr Ala Cys Thr Leu Ser Pro Gly Ser Pro Ala Gly Ser Ala Ser Asp
 180 185 190

Ala Glu His Trp Pro Pro Pro Arg Gly Arg Phe Ala Pro Pro Pro Pro
 195 200 205

Pro His Arg Cys Leu
 210

<210> 22
 <211> 450
 <212> DNA
 <213> MOUSE

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<210> 23
 <211> 149
 <212> PRT
 <213> MOUSE

<400> 23

Met Lys Ser Ala Cys Lys Pro His Gly Pro Pro Ala Gly Ala Arg Gly
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Ala Pro Pro Cys Ala Gly Ala Ala Glu Arg Ala Val Ser Cys Ala Gly
 20 25 30

Pro Gly Arg Leu Glu Ser Ala Ala Arg Arg Arg Leu Ala Ala Asn Ala
 35 40 45

Arg Glu Arg Arg Arg Met Gln Gly Leu Asn Thr Ala Phe Asp Arg Leu
 50 55 60

Arg Arg Val Val Pro Gln Trp Gly Gln Asp Lys Lys Leu Ser Lys Tyr

65		70		75		80
Glu Thr Leu Gln Met Ala Leu Ser Tyr Ile Ile Ala Leu Thr Arg Ile						
	85		90		95	
Leu Ala Glu Ala Glu Arg Asp Trp Val Gly Leu Arg Cys Glu Gln Arg						
	100		105		110	
Gly Arg Asp His Pro Tyr Leu Pro Phe Pro Gly Ala Arg Leu Gln Val						
	115		120		125	
Asp Pro Glu Pro Tyr Gly Gln Arg Leu Phe Gly Phe Gln Pro Glu Pro						
	130		135		140	
Phe Pro Met Ala Ser						
145						

<210> 24
 <211> 861
 <212> DNA
 <213> MOUSE

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<210> 25

<211> 214
 <212> PRT
 <213> MOUSE

<400> 25

Met Ala Pro His Pro Leu Asp Ala Leu Thr Ile Gln Val Ser Pro Glu
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Thr Gln Gln Pro Phe Pro Gly Ala Ser Asp His Glu Val Leu Ser Ser
 20 25 30

Asn Ser Thr Pro Pro Ser Pro Thr Leu Ile Pro Arg Asp Cys Ser Glu
 35 40 45

Ala Glu Val Gly Asp Cys Arg Gly Thr Ser Arg Lys Leu Arg Ala Arg
 50 55 60

Arg Gly Gly Arg Asn Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln
 65 70 75 80

Arg Arg Ser Arg Arg Lys Lys Ala Asn Asp Arg Glu Arg Asn Arg Met
 85 90 95

His Asn Leu Asn Ser Ala Leu Asp Ala Leu Arg Gly Val Leu Pro Thr
 100 105 110

Phe Pro Asp Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala
 115 120 125

His Asn Tyr Ile Trp Ala Leu Thr Gln Thr Leu Arg Ile Ala Asp His
 130 135 140

Ser Phe Tyr Gly Pro Glu Pro Pro Val Pro Cys Gly Glu Leu Gly Ser
 145 150 155 160

Pro Gly Gly Gly Ser Asn Gly Asp Trp Gly Ser Ile Tyr Ser Pro Val
 165 170 175

Ser Gln Ala Gly Asn Leu Ser Pro Thr Ala Ser Leu Glu Glu Phe Pro
 180 185 190

Gly Leu Gln Val Pro Ser Ser Pro Ser Tyr Leu Leu Pro Gly Ala Leu
 195 200 205

Val Phe Ser Asp Phe Leu
 210

<210> 26
<211> 72
<212> DNA
<213> MOUSE

<400> 26
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<210> 27
<211> 24
<212> PRT
<213> MOUSE

<400> 27
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Cys Tyr Ser Lys Thr Gln Lys Leu
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<210> 28
<211> 66
<212> DNA
<213> MOUSE

<400> 28
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<210> 29
<211> 22
<212> PRT
<213> MOUSE

<400> 29
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Cys Tyr Ser Lys Thr Gln
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<210> 30
<211> 1385
<212> DNA
<213> MOUSE

<400> 30
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<210> 31
 <211> 263
 <212> PRT
 <213> MOUSE

<400> 31

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			20					25					30		

Met Ser Ser Ser Ala Asp Glu Glu Glu Asp Glu Glu Leu Arg Arg Pro
 35 40 45
 Gly Ser Ala Arg Gly Gln Arg Gly Ala Glu Ala Glu Gln Gly Val Gln
 50 55 60
 Gly Ser Pro Ala Ser Gly Ala Gly Gly Cys Arg Pro Gly Arg Leu Leu
 65 70 75 80
 Gly Leu Met His Glu Cys Lys Arg Arg Pro Ser Arg Ser Arg Ala Val
 85 90 95
 Ser Arg Gly Ala Lys Thr Ala Glu Thr Val Gln Arg Ile Lys Lys Thr
 100 105 110
 Arg Arg Leu Lys Ala Asn Asn Arg Glu Arg Asn Arg Met His Asn Leu
 115 120 125
 Asn Ala Ala Leu Asp Ala Leu Arg Glu Val Leu Pro Thr Phe Pro Glu
 130 135 140
 Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala His Asn Tyr
 145 150 155 160
 Ile Trp Ala Leu Thr Glu Thr Leu Arg Leu Ala Asp His Cys Ala Gly
 165 170 175
 Ala Gly Gly Leu Gln Gly Ala Leu Phe Thr Glu Ala Val Leu Leu Ser
 180 185 190
 Pro Gly Ala Ala Leu Gly Ala Ser Gly Asp Ser Pro Ser Pro Pro Ser
 195 200 205
 Ser Trp Ser Cys Thr Asn Ser Pro Ala Ser Ser Ser Asn Ser Thr Ser
 210 215 220
 Pro Tyr Ser Cys Thr Leu Ser Pro Ala Ser Pro Gly Ser Asp Val Asp
 225 230 235 240
 Tyr Trp Gln Pro Pro Pro Pro Glu Lys His Arg Tyr Ala Pro His Leu
 245 250 255
 Pro Leu Ala Arg Asp Cys Ile
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<210> 32
 <211> 3541
 <212> DNA
 <213> MOUSE

<400> 32
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 caagatagag actcttcgac tggcaaggaa ctacatctgg gccttgtctg aagtcctgga 720
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 gaagcatgag gaaaaatctt caatttgtga ctctactatc tctgtccaca gcttcaacta 900
 tcagtctcca gggctcccca gccctcctta tggccatatg gaaacacatt ctctccatct 960
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 tccccccct tatgagggtc cactcacacc acccctgagc attagtggca acttctcctt 1080
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 gctttctgat aaacatgaag caactgttcc aaatcaacat atacctttca cctcccacac 1680

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tctaccaaac	tatatatgta	tctcttttct	ttattgccct	tatttatttc	ttcacactga	2820
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tataaatatg	tttaaaagtc	tgtaaagacg	tcttaaaaaa	ctcgtgacag	taattcacca	2940
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tgttctttta	ataatgttta	gtcttctggg	agtgttttca	gataaaatga	agcaattgtt	3480
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3541

<210> 33
 <211> 330
 <212> PRT
 <213> MOUSE

<400> 33

Met Ala Lys Met Tyr Met Lys Ser Lys Asp Met Val Glu Leu Val Asn
 1 5 10 15

Thr Gln Ser Trp Met Asp Lys Gly Leu Ser Ser Gln Asn Glu Met Lys
 20 25 30

Glu Gln Glu Arg Arg Pro Gly Ser Tyr Gly Met Leu Gly Thr Leu Thr
 35 40 45

Glu Glu His Asp Ser Ile Glu Glu Asp Glu Glu Glu Glu Glu Asp Gly
 50 55 60

Asp Lys Pro Lys Arg Arg Gly Pro Lys Lys Lys Lys Met Thr Lys Ala
 65 70 75 80

Arg Leu Glu Arg Phe Arg Ala Arg Arg Val Lys Ala Asn Ala Arg Glu
 85 90 95

Arg Thr Arg Met His Gly Leu Asn Asp Ala Leu Asp Asn Leu Arg Arg
 100 105 110

Val Met Pro Cys Tyr Ser Lys Thr Gln Lys Leu Ser Lys Ile Glu Thr
 115 120 125

Leu Arg Leu Ala Arg Asn Tyr Ile Trp Ala Leu Ser Glu Val Leu Glu
 130 135 140

Thr Gly Gln Thr Leu Glu Gly Lys Gly Phe Val Glu Met Leu Cys Lys
 145 150 155 160

Gly Leu Ser Gln Pro Thr Ser Asn Leu Val Ala Gly Cys Leu Gln Leu
 165 170 175

Gly Pro Gln Ser Thr Leu Leu Glu Lys His Glu Glu Lys Ser Ser Ile
 180 185 190

Cys Asp Ser Thr Ile Ser Val His Ser Phe Asn Tyr Gln Ser Pro Gly
 195 200 205

Leu Pro Ser Pro Pro Tyr Gly His Met Glu Thr His Ser Leu His Leu
 210 215 220

Lys Pro Gln Pro Phe Lys Ser Leu Gly Asp Ser Phe Gly Ser His Pro
 225 230 235 240

Pro Asp Cys Ser Thr Pro Pro Tyr Glu Gly Pro Leu Thr Pro Pro Leu
 245 250 255

Ser Ile Ser Gly Asn Phe Ser Leu Lys Gln Asp Gly Ser Pro Asp Leu
 260 265 270

Glu Lys Ser Tyr Asn Phe Met Pro His Tyr Thr Ser Ala Ser Leu Ser
 275 280 285

Ser Gly His Val His Ser Thr Pro Phe Gln Thr Gly Thr Pro Arg Tyr
 290 295 300

Asp Val Pro Val Asp Leu Ser Tyr Asp Ser Tyr Ser His His Ser Ile
 305 310 315 320

Gly Thr Gln Leu Asn Thr Ile Phe Ser Asp
 325 330

<210> 34
 <211> 800
 <212> DNA
 <213> MOUSE

<400> 34
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 agttttctga ccccccctct gttttgcctg ctctaccctg ccttgtagct ttctaatacac 180
 aagtcttttc agttccctta gttttcaccc atcaacttca gcagcccaca ccctctagtt 240
 ccttctggtg ttaaacaaaa acaaacacgc agtggcaaag ctggacctgg tcagagaagc 300
 tcccgccctg gtcagcagcc aaaaccagca aaacggcggc aagtcagaag ctccagtcag 420
 atcacaggag ctgcccagag actgtggtac tgaaagaact actcgcggga gctgaccccg 480
 ggaaagaggt actgaaaaga catagaaaac cagctgtggt ggaggcactg acatgaaggc 540
 atcctggtag tgcatacagaa ctccaggaaa aagtagaata agtaacagcc aaggtactca 600
 gaccaggaac agtcactaga aggtagctac cagtttaaca tggacgactg aaagggtctt 660

ctgtttccca cgatctgcct ggtcaggta gggtagaact gactgctctg atagttcttc 720
aggacacaga ttagagttaa atcttggaac tggacttcca gaggtgagcc tgtgaacggg 780
gtgtgggtac taaagtttct 800

<210> 35
<211> 515
<212> DNA
<213> CHICKEN

<400> 35
tttttctgta tgcgtgtgaa gctgcatctg caatagatat gaaaacctgt caatccagtc 60
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agtgcagcac agaaagaatg gagagcgtg ccaagagaag actggctgcc aacgccaggg 180
agagaagacg gatgcaagga ctgaacacag cttttgatcg tttgaggaag gtggttccac 240
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tcatggctct aacacgaata cttgctgaag cagagagata cagtactgaa agagaatgga 360
ttaaccttca ctgtgaacac tttcatccag agagctacca ccattatacg ggacaaaaag 420
tggcaacaga cagtgatcct tatgcacagc gaatattcag ctatcaccct gaacactttc 480
aaatagctaa ttagaactta ttacgagcta aaaaa 515

<210> 36
<211> 151
<212> PRT
<213> CHICKEN

<400> 36
Met Lys Thr Cys Gln Ser Ser His Leu Asp Ser Gly Val Glu Ser Asp
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Ile Gln Cys Arg Ser Gly Ser Gly Cys Val Val Lys Cys Ser Thr Glu
20 25 30
Arg Met Glu Ser Ala Ala Lys Arg Arg Leu Ala Ala Asn Ala Arg Glu
35 40 45
Arg Arg Arg Met Gln Gly Leu Asn Thr Ala Phe Asp Arg Leu Arg Lys
50 55 60
Val Val Pro Gln Trp Gly Gln Asp Lys Lys Leu Ser Lys Tyr Glu Thr
65 70 75 80
Leu Gln Met Ala Leu Ser Tyr Ile Met Ala Leu Thr Arg Ile Leu Ala
85 90 95

Glu Ala Glu Arg Tyr Ser Thr Glu Arg Glu Trp Ile Asn Leu His Cys
 100 105 110

Glu His Phe His Pro Glu Ser Tyr His His Tyr Thr Gly Gln Lys Val
 115 120 125

Ala Thr Asp Ser Asp Pro Tyr Ala Gln Arg Ile Phe Ser Tyr His Pro
 130 135 140

Glu His Phe Gln Ile Ala Asn
 145 150

<210> 37
 <211> 1412
 <212> DNA
 <213> MOUSE

<400> 37
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 gaagaggagg tactgatgct gctgggctcg gcttccccgg cctcggcgac cctgaccccg 180
 atgtcctcca gcgcggacga ggaggaggac gaggagctgc gccggccggg ctccgcgcgt 240
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 cactgcgccg gcgccggtgg cctccagggg gcgctcttca cggaggcggt gctcctgagc 660
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 tcttttcacc ttcgttttcta catagagatg ttaatgtcag tcgaaagaaa tgtatttttag 1320
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 tctattccca ttgctgtctg caggctgtgg ga 1412

<210> 38
 <211> 263
 <212> PRT
 <213> MOUSE

<400> 38

Met Phe Val Lys Ser Glu Thr Leu Glu Leu Lys Glu Glu Glu Glu Val
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Leu Met Leu Leu Gly Ser Ala Ser Pro Ala Ser Ala Thr Leu Thr Pro
 20 25 30

Met Ser Ser Ser Ala Asp Glu Glu Glu Asp Glu Glu Leu Arg Arg Pro
 35 40 45

Gly Ser Ala Arg Gly Gln Arg Gly Ala Glu Ala Gly Gln Gly Val Gln
 50 55 60

Gly Ser Pro Ala Ser Gly Ala Gly Gly Cys Arg Pro Gly Arg Leu Leu
 65 70 75 80

Gly Leu Met His Glu Cys Lys Arg Arg Pro Ser Arg Ser Arg Ala Val
 85 90 95

Ser Arg Gly Ala Lys Thr Ala Glu Thr Val Gln Arg Ile Lys Lys Thr
 100 105 110

Arg Arg Leu Lys Ala Asn Asn Arg Glu Arg Asn Arg Met His Asn Leu
 115 120 125

Asn Ala Ala Leu Asp Ala Leu Arg Glu Val Leu Pro Thr Phe Pro Glu
 130 135 140

Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala His Asn Tyr
 145 150 155 160

Ile Trp Ala Leu Thr Glu Thr Leu Arg Leu Ala Asp His Cys Ala Gly
 165 170 175

Ala Gly Gly Leu Gln Gly Ala Leu Phe Thr Glu Ala Val Leu Leu Ser
180 185 190

Pro Gly Ala Ala Leu Gly Ala Ser Gly Asp Ser Pro Ser Pro Pro Ser
195 200 205

Ser Trp Ser Cys Thr Asn Ser Pro Ala Ser Ser Ser Asn Ser Thr Ser
210 215 220

Pro Tyr Ser Cys Thr Leu Ser Pro Ala Ser Pro Gly Ser Asp Val Asp
225 230 235 240

Tyr Trp Gln Pro Pro Pro Pro Glu Lys His Arg Tyr Ala Pro His Leu
245 250 255

Pro Leu Ala Arg Asp Cys Ile
260

<210> 39
<211> 938
<212> DNA
<213> ZEBRA FISH

<400> 39
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caaaatatcc gtccctgtat ccatagccac aaactttcct cccaaaagca caaaccaaca 120
gaatggatgg aatgagcacg gatacaagag aggtggttga actcgacgtc cagcattcga 180
gcttggggcg gggggagcag agcaagtacc caccagcctt ggcactcatg gccagcagtg 240
accacgcgc ctggctggct ccctgacagg ctggcacctg cgcggcacac gccgaatacc 300
tgctgcactc gcccggtcgc agcgcggaag gcgtgtcctc tgccctcaac ttcaggaaga 360
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aggacggaac attcaactct ttcattggagc aagacctcca gtgcacctct ggaacgagca 840
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938

<210> 40
<211> 266
<212> PRT
<213> ZEBRA FISH

<400> 40

Met Asp Gly Met Ser Thr Asp Thr Arg Glu Val Val Glu Leu Asp Val
1 5 10 15

Gln His Ser Ser Leu Gly Arg Gly Glu Gln Ser Lys Tyr Pro Pro Ala
20 25 30

Leu Ala Leu Met Ala Ser Ser Asp Pro Arg Ala Trp Leu Ala Pro Val
35 40 45

Gln Ala Gly Thr Cys Ala Ala His Ala Glu Tyr Leu Leu His Ser Pro
50 55 60

Gly Ser Ser Ala Glu Gly Val Ser Ser Ala Ser Asn Phe Arg Lys Ser
65 70 75 80

Ser Lys Ser Pro Val Lys Val Arg Glu Leu Cys Arg Leu Lys Gly Ala
85 90 95

Val Gly Ala Asp Glu Gly Arg Gln Arg Ala Pro Ser Ser Lys Ser Thr
100 105 110

Asn Val Val Gln Lys Gln Arg Arg Met Ala Ala Asn Ala Arg Glu Arg
115 120 125

Arg Arg Met His Gly Leu Asn His Ala Phe Asp Glu Leu Arg Ser Val
130 135 140

Ile Pro Ala Phe Asp Asn Asp Lys Lys Leu Ser Lys Tyr Glu Thr Leu
145 150 155 160

Gln Met Ala Gln Ile Tyr Ile Asn Ala Leu Ser Asp Leu Leu Gln Gly
165 170 175

Pro Gly Ala Lys Ala Asp Pro Pro Asn Cys Asp Leu Leu His Ala Asn
180 185 190

Val Leu Glu Thr Asp Arg Ser Pro Arg Gly Ser Pro Gly Val Cys Arg
195 200 205

Arg Gly Thr Gly Val Gly Tyr Pro Tyr Gln Tyr Glu Asp Gly Thr Phe
 210 215 220

Asn Ser Phe Met Glu Gln Asp Leu Gln Ser Pro Ser Gly Thr Ser Lys
 225 230 235 240

Ser Gly Ser Glu Ala Ser Lys Asp Ser Pro Arg Ser Asn Arg Ser Asp
 245 250 255

Gly Glu Val Leu Ala Ser Leu Lys Cys Glu
 260 265

<210> 41
 <211> 948
 <212> DNA
 <213> FROG

<400> 41
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 atgaaggaga ggaatcagtc tgcctatgat atcatttcag gtctatgccca tgaggaaagg 120
 ggcagcattg atggagaaga ggatgatgaa gaagaagagg atggagagaa accaaaaaag 180
 aggggaccca aaaaaaagaa gatgaccaag gctagagtgg agaggttccg tgtccgtaga 240
 gtaaaagcca atgccaggga gcgttcaaga atgcatggac ttaatgatgc cctggaaaat 300
 ttgagaaggg ttatgccttg ctattccaaa acacaaaagt tgtctaaaat tgagactcct 360
 agactggcca gaaactatat atgggcatta tctgatattc tagaacaagg tcaaaatgca 420
 gagggaaagg gctttctgga aatactctgc aaaggctctt ctcagccaac aagcaactta 480
 gtagctggct gcttgcaact tggacctcag gccatgttct tggataaaca cgaagaaaag 540
 tctcatatat gtgattcctc tcttactggg catacttata attaccagtc cccaggacta 600
 cccagtcctc cttatggtaa cattgatgtt caccacttgc acttgaaacc ctcttctttc 660
 aaaccagtaa tggatccttc tgtggtaacc catacactta actgtaccac tccaccatat 720
 gaaggagctc taacacctcc actcagcatc ggtggtaatt tttctttgaa gcaagatagt 780
 tcacccgata tggataaata atatgcattc aggtccccct atccagctct tgggcttggt 840
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 gacatggctt acgagcctta cccacaccat gctatattca ctgaataa 948

<210> 42
 <211> 315
 <212> PRT
 <213> FROG

<400> 42

Met Ser Glu Met Val Asn Val His Gly Trp Met Glu Glu Ala Leu Ser
1 5 10 15

Ser Gln Asp Glu Met Lys Glu Arg Asn Gln Ser Ala Tyr Asp Ile Ile
20 25 30

Ser Gly Leu Cys His Glu Glu Arg Gly Ser Ile Asp Gly Glu Glu Asp
35 40 45

Asp Glu Glu Glu Glu Asp Gly Glu Lys Pro Lys Lys Arg Gly Pro Lys
50 55 60

Lys Lys Lys Met Thr Lys Ala Arg Val Glu Arg Phe Arg Val Arg Arg
65 70 75 80

Val Lys Ala Asn Ala Arg Glu Arg Ser Arg Met His Gly Leu Asn Asp
85 90 95

Ala Leu Glu Asn Leu Arg Arg Val Met Pro Cys Tyr Ser Lys Thr Gln
100 105 110

Lys Leu Ser Lys Ile Glu Thr Leu Arg Leu Ala Arg Asn Tyr Ile Trp
115 120 125

Ala Leu Ser Asp Ile Leu Glu Gln Gly Gln Asn Ala Glu Gly Lys Gly
130 135 140

Phe Leu Glu Ile Leu Cys Lys Gly Leu Ser Gln Pro Thr Ser Asn Leu
145 150 155 160

Val Ala Gly Cys Leu Gln Leu Gly Pro Gln Ala Met Phe Leu Asp Lys
165 170 175

His Glu Glu Lys Ser His Ile Cys Asp Ser Ser Leu Thr Gly His Thr
180 185 190

Tyr Asn Tyr Gln Ser Pro Gly Leu Pro Ser Pro Pro Tyr Gly Asn Ile
195 200 205

Asp Val His His Leu His Leu Lys Pro Ser Ser Phe Lys Pro Val Met
210 215 220

Asp Pro Ser Val Val Thr His Thr Leu Asn Cys Thr Thr Pro Pro Tyr
225 230 235 240

Glu Gly Ala Leu Thr Pro Pro Leu Ser Ile Gly Gly Asn Phe Ser Leu
 245 250 255

Lys Gln Asp Ser Ser Pro Asp Met Asp Lys Ser Tyr Ala Phe Arg Ser
 260 265 270

Pro Tyr Pro Ala Leu Gly Leu Gly Gly Ser His Gly His Ala Ser His
 275 280 285

Phe His Thr Ser Val Pro Arg Tyr Glu Leu Pro Ile Asp Met Ala Tyr
 290 295 300

Glu Pro Tyr Pro His His Ala Ile Phe Thr Glu
 305 310 315

<210> 43
 <211> 1550
 <212> DNA
 <213> MOUSE

<400> 43
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 caatgtgagg accagaaaca aattaagaaa ccagagagct ttccaaaaca agttgtcctt 180
 cgaggaaaga gcattaaaag ggcccctgga gaagaaaccg agaaagaaga ggaggaagaa 240
 gacagagagg aagaagatga gaatggcttg tccagaagga gggggctcag gaaaaaaaaag 300
 accaccaaac tacgactgga aagggtcaag ttcaggagac aggaagctaa tgcgcgcgag 360
 aggaaccgga tgcacggcct caatgatgct ctggacaatt tgcgaaaagt ggtcccctgt 420
 tactctaaaa cccaaaaact gtccaaaata gaaactttac gactggccaa aaattacatc 480
 tgggcacttt ctgaaattct gaggattggc aagagaccgg atctgctcac gttcgtccaa 540
 aacttatgca aaggtctttc ccagccaact acaaacttgg tggcaggctg cttacagctc 600
 aacgccagaa gtttctctgat gggtcagggt ggggaggctg cccaccacac aaggtcaccc 660
 tactccacat tctaccacc ctaccacagc cctgagctgg cactcccc agggcatggg 720
 actcttgata attccaagtc catgaaacct tacaattact gcagtgcata tgaatccttc 780
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 aattacaatt atggcatgca ttactgtgca gtgccacca ggggtcccct tgggcagggt 960
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 taaacagtgg tcattcacct cccactctaa ttaaggcaaa gcagatgctt gtgggctgag 1140
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<210> 44
 <211> 337
 <212> PRT
 <213> MOUSE

<400> 44

Met Leu Thr Leu Pro Phe Asp Glu Ser Val Val Met Pro Glu Ser Gln
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Met Cys Arg Lys Phe Ala Arg Gln Cys Glu Asp Gln Lys Gln Ile Lys
 20 25 30

Lys Pro Glu Ser Phe Pro Lys Gln Val Val Leu Arg Gly Lys Ser Ile
 35 40 45

Lys Arg Ala Pro Gly Glu Glu Thr Glu Lys Glu Glu Glu Glu Asp
 50 55 60

Arg Glu Glu Glu Asp Glu Asn Gly Leu Ser Arg Arg Arg Gly Leu Arg
 65 70 75 80

Lys Lys Lys Thr Thr Lys Leu Arg Leu Glu Arg Val Lys Phe Arg Arg
 85 90 95

Gln Glu Ala Asn Ala Arg Glu Arg Asn Arg Met His Gly Leu Asn Asp
 100 105 110

Ala Leu Asp Asn Leu Arg Lys Val Val Pro Cys Tyr Ser Lys Thr Gln
 115 120 125

Lys Leu Ser Lys Ile Glu Thr Leu Arg Leu Ala Lys Asn Tyr Ile Trp
 130 135 140

Ala Leu Ser Glu Ile Leu Arg Ile Gly Lys Arg Pro Asp Leu Leu Thr
 145 150 155 160

Phe Val Gln Asn Leu Cys Lys Gly Leu Ser Gln Pro Thr Thr Asn Leu
 165 170 175

Val Ala Gly Cys Leu Gln Leu Asn Ala Arg Ser Phe Leu Met Gly Gln
 180 185 190

Gly Gly Glu Ala Ala His His Thr Arg Ser Pro Tyr Ser Thr Phe Tyr
 195 200 205

Pro Pro Tyr His Ser Pro Glu Leu Ala Thr Pro Pro Gly His Gly Thr
 210 215 220

Leu Asp Asn Ser Lys Ser Met Lys Pro Tyr Asn Tyr Cys Ser Ala Tyr
 225 230 235 240

Glu Ser Phe Tyr Glu Ser Thr Ser Pro Glu Cys Ala Ser Pro Gln Phe
 245 250 255

Glu Gly Pro Leu Ser Pro Pro Pro Ile Asn Tyr Asn Gly Ile Phe Ser
 260 265 270

Leu Lys Gln Glu Glu Thr Leu Asp Tyr Gly Lys Asn Tyr Asn Tyr Gly
 275 280 285

Met His Tyr Cys Ala Val Pro Pro Arg Gly Pro Leu Gly Gln Gly Ala
 290 295 300

Met Phe Arg Leu Pro Thr Asp Ser His Phe Pro Tyr Asp Leu His Leu
 305 310 315 320

Arg Ser Gln Ser Leu Thr Met Gln Asp Glu Leu Asn Ala Val Phe His
 325 330 335

Asn

<210> 45
 <211> 1393
 <212> DNA
 <213> MOUSE

<400> 45
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 ggggcttata cccttcgttg aactgggttg ccagcacctc ctctaacacg gcacctccga 180
 gccattgcag tgcgatgtcc cgctgctgc atgcagaaga gtgggctgag gtaaaagagt 240
 tgggggacca ccacgccat cccagccgc accacgtccc gccgctgacg ccacagccac 300
 ctgctaccct gcaggcgaga gaccttcccg tctaccggc agaactgtcc ctctggata 360
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 ccagtatct gctgcattct cccgagctgg gtgcctccga ggccgcggcg ccccgggacg 480
 aggctgacag ccagggtgag ctggtaagga gaagcggctg tggcggcctc agcaagagcc 540
 ccggggccgt caaagtacgg gaacagctgt gcaagctgaa ggggtggggtt gtagtggacg 600
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<210> 46
 <211> 351
 <212> PRT
 <213> MOUSE

<400> 46

Met Ser Arg Leu Leu His Ala Glu Glu Trp Ala Glu Val Lys Glu Leu
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Gly Asp His His Arg His Pro Gln Pro His His Val Pro Pro Leu Thr
 20 25 30

Pro Gln Pro Pro Ala Thr Leu Gln Ala Arg Asp Leu Pro Val Tyr Pro
 35 40 45

Ala Glu Leu Ser Leu Leu Asp Ser Thr Asp Pro Arg Ala Trp Leu Thr
 50 55 60

Pro Thr Leu Gln Gly Leu Cys Thr Ala Arg Ala Ala Gln Tyr Leu Leu
 65 70 75 80

His Ser Pro Glu Leu Gly Ala Ser Glu Ala Ala Ala Pro Arg Asp Glu
 85 90 95

Ala Asp Ser Gln Gly Glu Leu Val Arg Arg Ser Gly Cys Gly Gly Leu
 100 105 110

Ser Lys Ser Pro Gly Pro Val Lys Val Arg Glu Gln Leu Cys Lys Leu
 115 120 125

Lys Gly Gly Val Val Val Asp Glu Leu Gly Cys Ser Arg Gln Arg Ala
 130 135 140

Pro Ser Ser Lys Gln Val Asn Gly Val Gln Lys Gln Arg Arg Leu Ala
 145 150 155 160

Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn His Ala Phe
 165 170 175

Asp Gln Leu Arg Asn Val Ile Pro Ser Phe Asn Asn Asp Lys Lys Leu
 180 185 190

Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile Asn Ala Leu
 195 200 205

Ser Glu Leu Leu Gln Thr Pro Asn Val Gly Glu Gln Pro Pro Pro Pro
 210 215 220

Thr Ala Ser Cys Lys Asn Asp His His His Leu Arg Thr Ala Ser Ser
 225 230 235 240

Tyr Glu Gly Gly Ala Gly Ala Ser Ala Val Ala Gly Ala Gln Pro Ala
 245 250 255

Pro Gly Gly Gly Pro Arg Pro Thr Pro Pro Gly Pro Cys Arg Thr Arg
 260 265 270

Phe Ser Gly Pro Ala Ser Ser Gly Gly Tyr Ser Val Gln Leu Asp Ala
 275 280 285

Leu His Phe Pro Ala Phe Glu Asp Arg Ala Leu Thr Ala Met Met Ala
 290 295 300

Gln Lys Asp Leu Ser Pro Ser Leu Pro Gly Gly Ile Leu Gln Pro Val
 305 310 315 320

Gln Glu Asp Asn Ser Lys Thr Ser Pro Arg Ser His Arg Ser Asp Gly
 325 330 335

Glu Phe Ser Pro His Ser His Tyr Ser Asp Ser Asp Glu Ala Ser
 340 345 350

<210> 47
 <211> 993
 <212> DNA
 <213> MOUSE

<400> 47
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 tatggaatgc tcggaacctt aactgaagag catgacagta ttgaggagga tgaagaagag 180
 gaagaagatg gagataaacc taaaagaaga ggtcccaaga aaaagaagat gactaaagct 240
 cgccttgaaa gattcagggc tcgaagagtc aaggccaatg ctagagaacg gacccggatg 300
 catggcctga atgatgcctt ggataatctt aggagagtca tgccatgtta ctctaaaact 360
 caaaagcttt ccaagataga gactcttcga ctggcaagga actacatctg ggccttgtct 420
 gaagtctctg agactgggtc gacacttgaa gggaagggat ttgtagagat gctatgtaaa 480
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 accctcctgg agaagcatga ggaaaaatct tcaatttgtg actctactat ctctgtccac 600
 agcttcaact atcagtctcc agggctcccc agccctcctt atggccatat ggaaacacat 660
 tctctccatc tcaagcctca accatttaag agtttgggtg actcttttgg gagccatcca 720
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 aacttctcct taaagcaaga cggctcccct gatttggaat aatcctacaa tttcatgcca 840
 cattatacct ctgcaagtct aagttcaggg catgtgcatt caactccctt tcagactggc 900
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<210> 48
 <211> 330
 <212> PRT
 <213> Mus musculus

<400> 48

Met Ala Lys Met Tyr Met Lys Ser Lys Asp Met Val Glu Leu Val Asn
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Thr Gln Ser Trp Met Asp Lys Gly Leu Ser Ser Gln Asn Glu Met Lys
 20 25 30

Glu Gln Glu Arg Arg Pro Gly Ser Tyr Gly Met Leu Gly Thr Leu Thr
 35 40 45

Glu Glu His Asp Ser Ile Glu Glu Asp Glu Glu Glu Glu Asp Gly
 50 55 60

Asp Lys Pro Lys Arg Arg Gly Pro Lys Lys Lys Lys Met Thr Lys Ala
 65 70 75 80

Arg Leu Glu Arg Phe Arg Ala Arg Arg Val Lys Ala Asn Ala Arg Glu
 85 90 95

Arg Thr Arg Met His Gly Leu Asn Asp Ala Leu Asp Asn Leu Arg Arg
 100 105 110

Val Met Pro Cys Tyr Ser Lys Thr Gln Lys Leu Ser Lys Ile Glu Thr
 115 120 125

Leu Arg Leu Ala Arg Asn Tyr Ile Trp Ala Leu Ser Glu Val Leu Glu
 130 135 140

Thr Gly Gln Thr Leu Glu Gly Lys Gly Phe Val Glu Met Leu Cys Lys
 145 150 155 160

Gly Leu Ser Gln Pro Thr Ser Asn Leu Val Ala Gly Cys Leu Gln Leu
 165 170 175

Gly Pro Gln Ser Thr Leu Leu Glu Lys His Glu Glu Lys Ser Ser Ile
 180 185 190

Cys Asp Ser Thr Ile Ser Val His Ser Phe Asn Tyr Gln Ser Pro Gly
 195 200 205

Leu Pro Ser Pro Pro Tyr Gly His Met Glu Thr His Ser Leu His Leu
 210 215 220

Lys Pro Gln Pro Phe Lys Ser Leu Gly Asp Ser Phe Gly Ser His Pro
 225 230 235 240

Pro Asp Cys Ser Thr Pro Pro Tyr Glu Gly Pro Leu Thr Pro Pro Leu
 245 250 255

Ser Ile Ser Gly Asn Phe Ser Leu Lys Gln Asp Gly Ser Pro Asp Leu
 260 265 270

Glu Lys Ser Tyr Asn Phe Met Pro His Tyr Thr Ser Ala Ser Leu Ser
 275 280 285

Ser Gly His Val His Ser Thr Pro Phe Gln Thr Gly Thr Pro Arg Tyr
 290 295 300

Asp Val Pro Val Asp Leu Ser Tyr Asp Ser Tyr Ser His His Ser Ile
 305 310 315 320

Gly Thr Gln Leu Asn Thr Ile Phe Ser Asp
 325 330

<210> 49
 <211> 2264
 <212> DNA
 <213> FROG

<400> 49
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 gatcactgca tatgaatgga ataaggagtg ctgctgctac ccaggctggg gtttgttccg 180
 agcccttcaa aaccttttgg ccatagaatc actgtgttga catgaagtca gattcaccag 240
 tgcattggga gtcccatact gaatgccagt caccatgccc actaagttgc atgccagcca 300
 ggctggaagg ctctaccaag agacgtctgg ctgccaatgc cagggaaaga aggagaatgc 360
 aaggactgaa taccgccttc gatagtctga ggaaagttgt accgcaatgg ggtgaggaca 420
 aaaaactttc caagtatgag actctacaga tggcactgag ctacatcatg gactaagca 480
 ggatcctcac ggaagcagaa agatacagca gaactgatcc aggggaatgg actaaaatgc 540
 actttgatca cattcaggaa gaacagtgcc tcagttatat gggagtgaga tgcccaagag 600
 actgtgatcg ctacctgccc cagacttttt ctactagga taggagatgt gagcaacagt 660
 cagcaggcaa ggtactatag acctgaagat agcagtgtat tcctacacac agcagccaat 720
 aatacaggga catttgcac atgggttatt tgtcatgtca ttctgcccc tgcactgctt 780

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atttcattaa gcacccaaag tcccaggact gggaatatat gtagggcacc ccacgtgatg      840
cagcccaaag tatgtgctgc tgcaactgat agtgagctgt gggacactgg aaaagcaaag      900
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cgtgtataaa attcctactg gtctcattct acttgtttct gtaagacaaa ccctgggtgtg    1440
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ttttttttca atgggcatga gttgtttatt tgtaaacaca gtcctaaagt taacagattg    1560
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gcaatatgca accctttaga attagaaaat gtagtacaac ggaacaaatg gtgaatggct    1680
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aatgtattgt tatctttcga aaaatgtgga tggaacgtga tcagggtgcaa attcatgcga    1920
tttacctgtg cataattcct ataaaacaga gacaatgtgt agttatagga ggattcacta    1980
cacggatgaa agatcttatt tacaacaggt taggcacaaa aagtcagga ccatgaaaaa    2040
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tcagcaccat attataatcc agcacaaggc agtaagtata aggctcccat actcttctca    2160
ctgataagct tgctagagat gttcccaagg aagcccatgt gctgccccatc ttctgcccct    2220
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<210> 50
<211> 138
<212> PRT
<213> FROG

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<400> 50

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Met Lys Ser Asp Ser Pro Val His Gly Glu Ser His Thr Glu Cys Gln
1           5           10           15

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Ser Pro Cys Pro Leu Ser Cys Met Pro Ala Arg Leu Glu Gly Ser Thr
 20 25 30

Lys Arg Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Gln Gly
 35 40 45

Leu Asn Thr Ala Phe Asp Ser Leu Arg Lys Val Val Pro Gln Trp Gly
 50 55 60

Glu Asp Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Leu Ser
 65 70 75 80

Tyr Ile Met Ala Leu Ser Arg Ile Leu Thr Glu Ala Glu Arg Tyr Ser
 85 90 95

Arg Thr Asp Pro Gly Glu Trp Thr Lys Met His Phe Asp His Ile Gln
 100 105 110

Glu Glu Gln Cys Leu Ser Tyr Met Gly Val Arg Cys Pro Arg Asp Cys
 115 120 125

Asp Arg Tyr Leu Pro Gln Thr Phe Ser His
 130 135

<210> 51
 <211> 2123
 <212> DNA
 <213> FROG

<400> 51
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 taaaaatgaa ataaggagat actaccagg ctgggggttta ttttgagtct ttcagaactt 180
 tctagggata gaatatctct gctgacatga agtcagattc accagtgcac agggagtccc 240
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 ccttcgatag tctgaggaaa gttgtaccac aatgggggtga agacaaacaa ctttccaaat 420
 atgagactct gcagatggcg ctgagctaca tcatggcact gagcaggatc ctctcggaag 480
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 tgccccagac tttttctcac taggataaga gcaggcaagg tactactgac ctgaagacag 660

cactgtttta atataatggg tcggttatac agcacccaat gatacaggga catttgcac	720
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ttcaggactg ggtacatatg tagggaaccc caagtgatgc agcccagagg atgcggtgct	840
gcaacggatg gcagttagt agctgtggaa cactggaaaa gccaaagtga ctggtatttt	900
gtgaaaggac atgcaagtta ttatgggttg catataatat ttacctccat acagcacagt	960
gatataactt cattgcctcc atcatacctg tgtgattata tataaaatgg tagttcctga	1020
gtcactactt tccatgttac ttatgcactg ttatcagata acatagagaa agtagtattt	1080
atacattaga aaaagtacta tatgtgcata taaattggcg tttaaagcag tctggataaa	1140
tcattttctg tggactcttt tcttacccca aggagccatt tatagttaa gtgctgctat	1200
aggcactgct cataagggaa aggaaacatt tttgtcactt gctgataata caaattgcat	1260
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tcaacaagag gtataattta catattttac cattttctgg cttctgtctg ctttttgaga	1380
gtggcaaatt acaacgtata taaaattcct acaggctcga atctacttgt tgctgtaaag	1440
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ttaaatattt ttatttgtaa tgggcgtcaa ttgtttattt gtaaacgcag ctccaaaaat	1560
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agtaagcaaa tctttgtaat tgaaattgta gtaaaactga acatatggtg aattgcttgg	1680
caatgtactg tatacatgct gacctataag ggctatgtag caaagtggg aaaaagtTTT	1740
ccctatcaaa atcactgcag gtttattggg ttgttgacaga tagaataata aaatctgaca	1800
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cctaacgagg caacttcagc acg	2123

<210> 52
 <211> 138
 <212> PRT
 <213> FROG

<400> 52

Met	Lys	Ser	Asp	Ser	Pro	Val	His	Arg	Glu	Ser	His	Thr	Gly	Cys	Gln
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Ser Pro Cys Pro Leu Arg Cys Leu Pro Ala Arg Leu Glu Gly Ser Thr
20 25 30

Lys Arg Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Gln Gly
35 40 45

Leu Asn Thr Ala Phe Asp Ser Leu Arg Lys Val Val Pro Gln Trp Gly
50 55 60

Glu Asp Lys Gln Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Leu Ser
65 70 75 80

Tyr Ile Met Ala Leu Ser Arg Ile Leu Ser Glu Ala Glu Arg Tyr Ser
85 90 95

Arg Thr Asp Pro Glu Glu Trp Thr Asn Ile Gln Tyr Asp His Ile Glu
100 105 110

Glu Glu Gln Cys Leu Ser Tyr Met Glu Val Arg Cys Pro Arg Asp Cys
115 120 125

Asp Arg Tyr Leu Pro Gln Thr Phe Ser His
130 135

<210> 53
<211> 136
<212> DNA
<213> BEETLE

<400> 53
gcggcgaatg cgcgcgagcg gcggcggatg aacggcctga atgaagcttt cgatcggcta 60
agacaagtta taccaagctt ggacgctgac cacaaattga gcaagtttga gactctgcag 120
atggcccaga cctaca 136

<210> 54
<211> 45
<212> PRT
<213> BEETLE

<400> 54

Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Asn Gly Leu Asn Glu Ala
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Phe Asp Arg Leu Arg Gln Val Ile Pro Ser Leu Asp Ala Asp His Lys
20 25 30

Leu Ser Lys Phe Glu Thr Leu Gln Met Ala Gln Thr Tyr
 35 40 45

<210> 55
 <211> 137
 <212> DNA
 <213> BEETLE

<400> 55
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 cgggacgtgg tgccgtccct tgggaacgat cggaagctgt ccaagtttga gacacttcag 120
 atggcccaga cctacat 137

<210> 56
 <211> 45
 <212> PRT
 <213> BEETLE

<400> 56

Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Asn Ser Leu Asn Asp Ala
 1 5 10 15

Phe Asp Arg Leu Arg Asp Val Val Pro Ser Leu Gly Asn Asp Arg Lys
 20 25 30

Leu Ser Lys Phe Glu Thr Leu Gln Met Ala Gln Thr Tyr
 35 40 45

<210> 57
 <211> 1572
 <212> DNA
 <213> HUMAN

<220>
 <221> misc_feature
 <222> (1497)..(1564)
 <223> n can be any nucleotide

<400> 57
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 ggagaggagc ggggggagac tgagtggcgc gtgccgcttt ttaaaggggc gcagcgcctt 180
 cagcaaccgg agaagcatag ttgcacgcga cctggtgtgt gatctccgag tgggtggggg 240
 agggctcgagg agggaaaaaa aaataagacg ttgcagaaga gacccggaaa gggccttttt 300
 tttggttgag ctggtgtccc agtgctgcct ccgatcctga gcgtccgagc ctttgagtg 360

caatgtcccg cctgctgcat gcagaagagt gggctgaagt gaaggagttg ggagaccacc 420
 atcgccagcc ccagccgcat catctccgc aaccgccgc gccgccgag ccacctgcaa 480
 ctttgcaggc gagagagcat cccgtctacc cgctgagct gtccctcctg gacagcaccg 540
 acccagcgcg ctggctggct ccactttgc agggcatctg caccggcacgc gccgcccagt 600
 atttgctaca ttccccggag ctgggtgcct cagaggccgc tgcgccccgg gacgaggtgg 660
 acggccgggg ggagctggta aggaggagca gcggcggtgc cagcagcagc aagagccccg 720
 ggccggtgaa agtgcgggaa cagctgtgca agctgaaagg cggggtggtg gtagacgagc 780
 tgggctgcag ccgccaacgg gcccttcca gcaaacaggt gaatggggtg cagaagcaga 840
 gacggctagc agccaacgcc agggagcggc gcaggatgca tgggctgaac caccgcttcg 900
 accagctgcg caatgttatc ccgtcgttca acaacgacaa gaagctgtcc aaatatgaga 960
 ccctgcagat ggcccaaadc tacatcaacg ccttgctcga gctgctacaa acgcccagcg 1020
 gaggggaaca gccaccgccg cctccagcct cctgcaaaag cgaccaccac caccttcgca 1080
 ccgcggcctc ctatgaaggg ggcgcgggca acgcgaccgc agctggggct cagcaggctt 1140
 ccggagggag ccagcgggcg accccgcccg ggagttgccg gactcgcttc tcagccccag 1200
 cttctgcggg agggctactcg gtgcagctgg acgctctgca cttctcgact ttcgaggaca 1260
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 aattttcccc ccattcccat tacagtgact cggatgaggg aagttaggaa ggtgacagaa 1440
 gcctgaaaac tgagacagaa aaaaaactgc ctttccagag tgcgcgggaa gccccnggt 1500
 taangatccc cgcacccttt aatttnggct ctgcgatggc cgttgttttag caacgacttg 1560
 gctncagatg gt 1572

<210> 58
 <211> 354
 <212> PRT
 <213> HUMAN

<400> 58

Met Ser Arg Leu Leu His Ala Glu Glu Trp Ala Glu Val Lys Glu Leu
 1 5 10 15

Gly Asp His His Arg Gln Pro Gln Pro His His Leu Pro Gln Pro Pro
 20 25 30

Pro Pro Pro Gln Pro Pro Ala Thr Leu Gln Ala Arg Glu His Pro Val
 35 40 45

Tyr Pro Pro Glu Leu Ser Leu Leu Asp Ser Thr Asp Pro Arg Ala Trp
 50 55 60

Leu Ala Pro Thr Leu Gln Gly Ile Cys Thr Ala Arg Ala Ala Gln Tyr
 65 70 75 80

Leu Leu His Ser Pro Glu Leu Gly Ala Ser Glu Ala Ala Ala Pro Arg
 85 90 95

Asp Glu Val Asp Gly Arg Gly Glu Leu Val Arg Arg Ser Ser Gly Gly
 100 105 110

Ala Ser Ser Ser Lys Ser Pro Gly Pro Val Lys Val Arg Glu Gln Leu
 115 120 125

Cys Lys Leu Lys Gly Gly Val Val Val Asp Glu Leu Gly Cys Ser Arg
 130 135 140

Gln Arg Ala Pro Ser Ser Lys Gln Val Asn Gly Val Gln Lys Gln Arg
 145 150 155 160

Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn
 165 170 175

180 185 190

Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile
 195 200 205

Asn Ala Leu Ser Glu Leu Leu Gln Thr Pro Ser Gly Gly Glu Gln Pro
 210 215 220

Pro Pro Pro Pro Ala Ser Cys Lys Ser Asp His His His Leu Arg Thr
 225 230 235 240

Ala Ala Ser Tyr Glu Gly Gly Ala Gly Asn Ala Thr Ala Ala Gly Ala
 245 250 255

Gln Gln Ala Ser Gly Gly Ser Gln Arg Pro Thr Pro Pro Gly Ser Cys
 260 265 270

Arg Thr Arg Phe Ser Ala Pro Ala Ser Ala Gly Gly Tyr Ser Val Gln
 275 280 285

Leu Asp Ala Leu His Phe Ser Thr Phe Glu Asp Ser Ala Leu Thr Ala
 290 295 300

Met Met Ala Gln Lys Asn Leu Ser Pro Ser Leu Pro Gly Ser Ile Leu
 305 310 315 320

Gln Pro Val Gln Glu Glu Asn Ser Lys Thr Ser Pro Arg Ser His Arg
 325 330 335

Ser Asp Gly Glu Phe Ser Pro His Ser His Tyr Ser Asp Ser Asp Glu
 340 345 350

Ala Ser

<210> 59
 <211> 485
 <212> DNA
 <213> CHICKEN

<220>
 <221> misc_feature
 <222> (147)..(147)
 <223> n can be any nucleotide

<400> 59
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 aggcggcccc tggcgggggg cgcggnccgc gttccggcgg gagcagcccc gggggagcgc 180
 ggggcggcgg cgggcgcgcg gggcggcggc ggcggggccg ggccgcgggc gcaggtgagc 240
 ggcgtgcaga agcagcggcg gctggcggcc aacgcgcggg agcggcggcg gatgcacggg 300
 ctgaaccacg ccttcgacca gctgcgtaat gtcatccctt ccttcaacaa cgacaagaag 360
 ctctccaagt acgagacgct gcagatggcg caaatctaca tcagcgcctt cgccgagctg 420
 ctgcacgggc cgcccgcgcc ccccgagccg cccgccaagg ccgagctccg cggggccccc 480
 ttcga 485

<210> 60
 <211> 161
 <212> PRT
 <213> CHICKEN

<400> 60

Pro Leu Leu Gly Pro Asp Gly Ala Ala Ala Ser Pro Pro Ala Gly
 1 5 10 15

Trp Ala Cys Ala Ala Pro His Ala Cys Pro Pro Arg Arg Arg Ala Thr

20

25

30

Cys Cys Pro Pro Thr Arg Arg Thr Arg Arg Pro Val Ala Gly Gly Ala
35 40 45

Ala Arg Val Pro Ala Gly Ala Ala Pro Gly Glu Arg Gly Ala Ala Ala
50 55 60

Gly Ala Arg Gly Gly Gly Gly Gly Ala Gly Pro Arg Ala Gln Val Ser
65 70 75 80

Gly Val Gln Lys Gln Arg Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg
85 90 95

Arg Met His Gly Leu Asn His Ala Phe Asp Gln Leu Arg Asn Val Ile
100 105 110

Pro Ser Phe Asn Asn Asp Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln
115 120 125

Met Ala Gln Ile Tyr Ile Ser Ala Leu Ala Glu Leu Leu His Gly Pro
130 135 140

Pro Ala Pro Pro Glu Pro Pro Ala Lys Ala Glu Leu Arg Gly Ala Pro
145 150 155 160

Phe

<210> 61
<211> 138
<212> DNA
<213> PUFFER FISH

<400> 61
gcggcgaacg cgagggagag gaggagaatg cacggcctga ataaagcgtt tgacgaactg 60
aggagcgtca ttccttcctt ggaaaatgag agaaagctct ccaagtatga cactctccag 120
atggcccaaa cctacatc 138

<210> 62
<211> 46
<212> PRT
<213> PUFFER FISH

Ala Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn Lys Ala
1 5 10 15

Phe Asp Glu Leu Arg Ser Val Ile Pro Ser Leu Glu Asn Glu Arg Lys
 20 25 30

Leu Ser Lys Tyr Asp Thr Leu Gln Met Ala Gln Thr Tyr Ile
 35 40 45

<210> 63
 <211> 1477
 <212> DNA
 <213> DROSOPHILA

<400> 63
 atcatcttgt tagcggttt agagccgaat cgttttctag cgccatttta agctcgcaac 60
 gaactgaggt ataaccgggc tctctgagac cgctgcaact caccaccaac tgccatttgt 120
 cgtgccactc gggcggcacg tgctgccttc tgtggcaact cgtttacctg cccccctacc 180
 tgcctttcag gcccttctga ccgtcgtggt ggatttgtga gtataaatag ggccgaaagg 240
 acgagagacc agtcagaaac ccgccagcac tcgcagcggt cgtatcgttt catccagcaa 300
 cataacacca ccatacagca gcagcaacat gtcgtccagt gagatctatc gctactacta 360
 caagacctcc gaggacttgc agggcttcaa gacagccgcc gccgagccgt acttcaatcc 420
 catggcagcc tacaatcccg gcgtgacca ctaccagttc aatggcaaca ccctggccag 480
 cagcagcaac tacttgtcgg ccaatggctt catcagcttc gagcaggcca gttccgatgg 540
 ctggatctcc tcctcgccgg ctagccaccg atctgagagt cccgagtatg tggatctcaa 600
 taccatgtac aatggaggct gcaacaacat ggcccagaac caacaatacg gaatgattat 660
 ggagcagtct gttgtttcca cagcgcctgc aattccagtg gcctctcttc cggcagtgga 720
 ggtcatgggc tcctccaacg tgggcacttg caaacgatt ccagcctcag cagctccgaa 780
 accgaagcgt agctatacca agaagaacca gccaaagcacc accgccacct ccacaccgac 840
 tgcagctgcg gagtcatctg cctcagtga tctctacacg gaggagtcc agaactttga 900
 ctttgacaac tccgccttgt tcgatgacag cgtcgaggat gacgaggacc tcatgctctt 960
 cagtggcggg gaggacttcg atggcaatga tggatccttt gacttggccg atggtgagaa 1020
 ccaagatgcc gctgccggag gctctggaaa gaagaggcgt ggcaagcaga tcacaccgct 1080
 cgtgaagagg aagcgtcgcc tggccgcaa tgcacgtgag cgtcgtcgga tgcagaacct 1140
 caaccaggcc ttcgatcgtc tccgccagta cttccctgt ctgggaaacg atcgccagct 1200
 gtccaaacac gagaccctcc aaatggccca gacctacata tccgctctcg gggatctgct 1260
 gcgctgaatt cccggatccc gatcccagtc ccaagtacta ttctcagtta ttgttgagc 1320
 ttgccaaatg ttgtagctac tttgtatata ttgcctggag cccagtagtg aattaccgct 1380

taagtattat gctgtttatt gtttagttaa ttagcctaaa tggaagacaa tgattaagac 1440

taaggaagac aaaataaaaag caccattaat aatttaa 1477

<210> 64
<211> 312
<212> PRT
<213> DROSOPHILA

<400> 64

Met Ser Ser Ser Glu Ile Tyr Arg Tyr Tyr Tyr Lys Thr Ser Glu Asp
1 5 10 15

Leu Gln Gly Phe Lys Thr Ala Ala Ala Glu Pro Tyr Phe Asn Pro Met
20 25 30

Ala Ala Tyr Asn Pro Gly Val Thr His Tyr Gln Phe Asn Gly Asn Thr
35 40 45

Leu Ala Ser Ser Ser Asn Tyr Leu Ser Ala Asn Gly Phe Ile Ser Phe
50 55 60

Glu Gln Ala Ser Ser Asp Gly Trp Ile Ser Ser Ser Pro Ala Ser His
65 70 75 80

Arg Ser Glu Ser Pro Glu Tyr Val Asp Leu Asn Thr Met Tyr Asn Gly
85 90 95

Gly Cys Asn Asn Met Ala Gln Asn Gln Gln Tyr Gly Met Ile Met Glu
100 105 110

Gln Ser Val Val Ser Thr Ala Pro Ala Ile Pro Val Ala Ser Pro Pro
115 120 125

Ala Val Glu Val Met Gly Ser Ser Asn Val Gly Thr Cys Lys Thr Ile
130 135 140

Pro Ala Ser Ala Ala Pro Lys Pro Lys Arg Ser Tyr Thr Lys Lys Asn
145 150 155 160

Gln Pro Ser Thr Thr Ala Thr Ser Thr Pro Thr Ala Ala Ala Glu Ser
165 170 175

Ser Ala Ser Val Asn Leu Tyr Thr Glu Glu Phe Gln Asn Phe Asp Phe
180 185 190

Asp Asn Ser Ala Leu Phe Asp Asp Ser Val Glu Asp Asp Glu Asp Leu

195	200	205
Met Leu Phe Ser Gly Gly Glu Asp Phe Asp Gly Asn Asp Gly Ser Phe		
210	215	220
Asp Leu Ala Asp Gly Glu Asn Gln Asp Ala Ala Ala Gly Gly Ser Gly		
225	230	235
Lys Lys Arg Arg Gly Lys Gln Ile Thr Pro Val Val Lys Arg Lys Arg		
	245	250
Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Gln Asn Leu Asn		
	260	265
Gln Ala Phe Asp Arg Leu Arg Gln Tyr Leu Pro Cys Leu Gly Asn Asp		
	275	280
Arg Gln Leu Ser Lys His Glu Thr Leu Gln Met Ala Gln Thr Tyr Ile		
	290	295
Ser Ala Leu Gly Asp Leu Leu Arg		
305	310	

<210> 65
 <211> 907
 <212> DNA
 <213> FROG

<400> 65	
gccccggggc cactctgcgc acttgctcggg acttattcgc acttacctgt catggcccgt	60
ctgctacacg gcgctgctac tgccgctgac tggctgcgagc tgaaggagct tccatccgag	120
gccacttccc tgcaaagtcg ccctgagtac gtgctgcacc ccccgggccg ggccggggcgc	240
acaaggtgcg ggaactgtgc aaactgaagg ggctgcggga tgatgatgat gatgaggagg	300
atgatgagga ggaggaagag agatccgagg ggctgtgcag acacaggggt cccctggca	360
agggccctgg tggggttcag aagcagagga gactggcagc caatgccagg gagaggagga	420
ggatgcacgg gctcaatcat gccttcgatc agctccgtaa tgtcatccct tccttcaata	480
acgacaagaa actctccaaa tacgagaccc tgcagatggc tcagatctac atcaacgccc	540
tgtccgacct gctgcaggcg ccccccgact ccagagatcc cccctgcccg cccacctacc	600
aactgcattc ggggccagag cccaggttag tccagtctgg cagcatgaga ttctcggaga	660
cttccccccg acagtcccc ctcagccaat tccaggaggg agctgctccc agaaggggaat	720
aggatctggg cccatcttca tcttctcggg aagacatcgc ccattctcat cttcggggag	780

aagacagcaa gacatcgcaa gatctcatcg gagtgacggc gaattccggt ctccctatag 840
 tgagtcgtat taatttcgat aagccagctg cattaatgaa tcggccaaac gcgcggggag 900
 aggcggt 907

<210> 66
 <211> 259
 <212> PRT
 <213> FROG

<400> 66

Met Ala Arg Leu Leu His Gly Ala Ala Thr Ala Ala Asp Trp Cys Glu
 1 5 10 15

Leu Lys Glu Leu Pro Ser Glu Ala Gly Leu Leu Ala Arg Asp Tyr Leu
 20 25 30

Leu Asp Ser Ser Asp Pro Arg Ala Trp Leu Ser Ala Thr Ser Leu Gln
 35 40 45

Ser Arg Pro Glu Tyr Val Leu His Pro Pro Gly Arg Ala His Lys Val
 50 55 60

Arg Glu Leu Cys Lys Leu Lys Gly Leu Arg Asp Asp Asp Asp Asp Glu
 65 70 75 80

Glu Glu Asp Asp Glu Glu Glu Glu Glu Arg Ser Glu Gly Leu Cys Arg
 85 90 95

His Arg Gly Pro Pro Gly Lys Gly Pro Gly Gly Val Gln Lys Gln Arg
 100 105 110

Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn
 115 120 125

His Ala Phe Asp Gln Leu Arg Asn Val Ile Pro Ser Phe Asn Asn Asp
 130 135 140

Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile
 145 150 155 160

Asn Ala Leu Ser Asp Leu Leu Gln Ala Pro Pro Asp Ser Arg Asp Pro
 165 170 175

Pro Cys Pro Pro Thr Tyr Gln Leu His Ser Gly Pro Glu Pro Arg Leu
 180 185 190

Val Gln Ser Gly Ser Cys Met Arg Phe Ser Gly Asp Phe Pro Gly Gln
 195 200 205

Ser Pro Leu Ser Phe Gln Phe Gln Glu Gly Ala Ala Leu Ser Gly Lys
 210 215 220

Gly Ile Gly Ser Ala Pro Ser Ser Ser Ser Gly Glu Asp Ser Lys Thr
 225 230 235 240

Ser Pro Arg Ser His Arg Ser Asp Gly Glu Phe Arg Ser Pro Tyr Ser
 245 250 255

Glu Ser Tyr

<210> 67
 <211> 19
 <212> DNA
 <213> SYNTHETIC CONSTRUCT

<400> 67
 tgaagctttt ggctttgag 19

<210> 68
 <211> 19
 <212> DNA
 <213> SYNTHETIC CONSTRUCT

<400> 68
 ccgctgccaa attctttgg 19

<210> 69
 <211> 37
 <212> DNA
 <213> HUMAN

<400> 69
 gggggcactg acagtaatgc atgccgtatt cgaagtt 37

<210> 70
 <211> 21
 <212> PRT
 <213> HUMAN

<400> 70

Ala Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn His Ala
 1 5 10 15

Phe Asp Gln Leu Arg

